



## SEQUENCE LISTING

<110> Meagher, Richard B.  
Laterza, Vince

<120> RAPID PRODUCTION OF MONOCLONAL  
ANTIBODIES

<130> 21099.0074U2

<140> 10/079,130  
<141> 2002-02-20

<150> 60/270,322  
<151> 2001-02-20

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 681  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 1  
aagcttgc a ccatgccagg gggcttagaa gcccctcagag ccctgcctct cctcctcttc 60  
ttgtcatacg cctgtttggg tcccgatgc caggccctgc gggtagaagg gggtccacca 120  
tccctgacgg tgaacttggg cgaggaggcc cgcctcacct gtaaaaacaa tggcaggaac 180  
cctaataatca catggtgggtt cagccttcag tctaataatca catggccccc agtgcactg 240  
ggtcctggcc agggtaccac agggcagctg ttcttccccg aagtaaaacaa gaaccacagg 300  
ggcttgtact ggtgccaagt gatagaaaaac aacatattaa aacgctcctg tggtacttac 360  
ctccgcgtgc gcaatccagt ccctaggccc ttccctggaca tgggggaagg taccagaac 420  
cgcacatcatca cagcagaagg gatcatctt cttgtgtgt cagtggtgcc agggacgctg 480  
ctgttattca gaaacgggt gcaaaatgag aagtttgggg tggacatgcc agatgactat 540  
gaagataaaa atctctatga gggcctgaac cttgtatgact gttctatgtt tgaggacatc 600  
tccaggggac tccaggggcac ctaccaggat gtggcaacc tccacattgg agatgcccag 660  
ctggaaaagg catgagaatt c 681

<210> 2

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 2  
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ctgctgctgc tcttctcagg tgagccggta ccagcaatga caagcagtga cctgccactg 120  
aatttccaag gaagcccttg ttcccgatgc tggcagcacc cgagggttgc agccaaaaag 180  
cgagctcca tggtaagtt tcactgctac acaaaccact caggtgcact gacctgggtc 240  
cgaaagcgag ggagccagca gccccaggaa ctggtctcag aagagggacg cattgtgcag 300  
acccagaatg gctctgtcta caccctcact atccaaaaca tccagtagca ggataatgg 360  
atctacttct gcaagcagaa atgtgacacgc gccaaccata atgtcaccga cagctgtggc 420

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acggaaacttc tagtcttagg attcagcacg ttggaccaac tgaagcggcg	gaacacactg	480
aaagatggca ttatcttcat ccagaccctc ctcatcatcc tcttcatcat	tgtgcccata	540
ttcctgctac ttgacaagga tgacggcaag gctgggatcg aggaagatca	caccatgag	600
ggcttgaaca ttgaccagac agccacctat gaagacatag tgactctcg	gacaggggag	660
gtaaagtggc cggttaggaga gcatccaggc caggaatgac tcgag		705

&lt;210&gt; 3

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 3

Met Pro Gly Gly Leu Glu Ala Leu Arg Ala Leu Pro Leu Leu Leu Phe		
1 5 10 15		
Leu Ser Tyr Ala Cys Leu Gly Pro Gly Cys Gln Ala Leu Arg Val Glu		
20 25 30		
Gly Gly Pro Pro Ser Leu Thr Val Asn Leu Gly Glu Glu Ala Arg Leu		
35 40 45		
Thr Cys Glu Asn Asn Gly Arg Asn Pro Asn Ile Thr Trp Trp Phe Ser		
50 55 60		
Leu Gln Ser Asn Ile Thr Trp Pro Pro Val Pro Leu Gly Pro Gly Gln		
65 70 75 80		
Gly Thr Thr Gly Gln Leu Phe Phe Pro Glu Val Asn Lys Asn His Arg		
85 90 95		
Gly Leu Tyr Trp Cys Gln Val Ile Glu Asn Asn Ile Leu Lys Arg Ser		
100 105 110		
Cys Gly Thr Tyr Leu Arg Val Arg Asn Pro Val Pro Arg Pro Phe Leu		
115 120 125		
Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala Glu Gly Ile		
130 135 140		
Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu Leu Phe Arg		
145 150 155 160		
Lys Arg Trp Gln Asn Glu Lys Phe Gly Val Asp Met Pro Asp Asp Tyr		
165 170 175		
Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn Leu Asp Asp Cys Ser Met		
180 185 190		
Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly Thr Tyr Gln Asp Val Gly		
195 200 205		
Asn Leu His Ile Gly Asp Ala Gln Leu Glu Lys Pro		
210 215 220		

&lt;210&gt; 4

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 4

Met Ala Thr Leu Val Leu Ser Ser Met Pro Cys His Trp Leu Leu Phe		
1 5 10 15		
Leu Leu Leu Leu Phe Ser Gly Glu Pro Val Pro Ala Met Thr Ser Ser		
20 25 30		

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Asp Leu Pro Leu Asn Phe Gln Gly Ser Pro Cys Ser Gln Ile Trp Gln  
35 40 45  
His Pro Arg Phe Ala Ala Lys Lys Arg Ser Ser Met Val Lys Phe His  
50 55 60  
Cys Tyr Thr Asn His Ser Gly Ala Leu Thr Trp Phe Arg Lys Arg Gly  
65 70 75 80  
Ser Gln Gln Pro Gln Glu Leu Val Ser Glu Glu Gly Arg Ile Val Gln  
85 90 95  
Thr Gln Asn Gly Ser Val Tyr Thr Leu Thr Ile Gln Asn Ile Gln Tyr  
100 105 110  
Glu Asp Asn Gly Ile Tyr Phe Cys Lys Gln Lys Cys Asp Ser Ala Asn  
115 120 125  
His Asn Val Thr Asp Ser Cys Gly Thr Glu Leu Leu Val Leu Gly Phe  
130 135 140  
Ser Thr Leu Asp Gln Leu Lys Arg Arg Asn Thr Leu Lys Asp Gly Ile  
145 150 155 160  
Ile Leu Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile  
165 170 175  
Phe Leu Leu Leu Asp Lys Asp Asp Gly Lys Ala Gly Met Glu Glu Asp  
180 185 190  
His Thr Tyr Glu Gly Leu Asn Ile Asp Gln Thr Ala Thr Tyr Glu Asp  
195 200 205  
Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu His  
210 215 220  
Pro Gly Gln Glu  
225